

SEQUENCE LISTING

<110> Goodearl, Andrew
Glucksmann, Alexandra M.

<120> OCT1P, A PROTEIN HAVING HOMOLOGY TO THE ORGANIC AND SUGAR
TRANSPORTER FAMILY OF PROTEINS, AND USES THEREOF

<130> 07334/130001

<140> US 09/342,959
<141> 1999-06-29

<150> US 09/107,932
<151> 1998-06-30

<160> 20

<170> FastSEQ for Windows Version 3.0

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<212> DNA
<213> Homo sapiens

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<221> misc_feature
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ggctcgtcat ccaccactac catgtaaggg ccatgagaag ggctcatcct ggcgagcgcg	180
ggac atg gag gag gac tta ttc cag cta agg cag ctg ccg gtt gtg aaa	229
Met Glu Glu Asp Leu Phe Gln Leu Arg Gln Leu Pro Val Val Lys	
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ttc cgt cgc aca ggc gag agt gca agg tca gag gac gac acg gct tca	277
Phe Arg Arg Thr Gly Glu Ser Ala Arg Ser Glu Asp Asp Thr Ala Ser	
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gga gag cat gaa gtc cag att gaa ggg gtc cac gtg ggc cta gag gct	325
Gly Glu His Glu Val Gln Ile Glu Gly Val His Val Gly Leu Glu Ala	
35 40 45	
gtg gag ctg gat gat ggg gca gct gtg ccc aag gag ttt gcc aat ccc	373
Val Glu Leu Asp Asp Gly Ala Ala Val Pro Lys Glu Phe Ala Asn Pro	
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acc gat gat act ttc atg gtg gaa gat gca gtg gaa gcc att ggc ttt	421
Thr Asp Asp Thr Phe Met Val Glu Asp Ala Val Glu Ala Ile Gly Phe	
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gga aaa ttt cag tgg aag ctg tct gtt ctc act ggc ttg gct tgg atg	469
Gly Lys Phe Gln Trp Lys Leu Ser Val Leu Thr Gly Leu Ala Trp Met	
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000465 02404

gct gat gcc atg gag atg atg atc ctc agc atc ctg gca cca cag ctg	517
Ala Asp Ala Met Glu Met Met Ile Leu Ser Ile Leu Ala Pro Gln Leu	
100 105 110	
cat tgc gag tgg agg ctc cca agc tgg cag gtg gca ttg ctg acc tcg	565
His Cys Glu Trp Arg Leu Pro Ser Trp Gln Val Ala Leu Leu Thr Ser	
115 120 125	
gtg gtc ttt gta ggc atg atg tcc agc tcc acg ctc tgg gga aat atc	613
Val Val Phe Val Gly Met Met Ser Ser Ser Thr Leu Trp Gly Asn Ile	
130 135 140	
tca gac cag tac ggc agg aaa aca ggg ctg aag atc agc gtg ctg tgg	661
Ser Asp Gln Tyr Gly Arg Lys Thr Gly Leu Lys Ile Ser Val Leu Trp	
145 150 155	
act ctg tac tat ggc atc ctt agt gca ttt gcg ccc gtg tat agc tgg	709
Thr Leu Tyr Tyr Gly Ile Leu Ser Ala Phe Ala Pro Val Tyr Ser Trp	
160 165 170 175	
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Ile Leu Val Leu Arg Gly Leu Val Gly Phe Gly Ile Gly Gly Val Pro	
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cag tcg gtg acg ctg tat gcc gag ttc ctt ccc atg aaa gcc aga gct	805
Gln Ser Val Thr Leu Tyr Ala Glu Phe Leu Pro Met Lys Ala Arg Ala	
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aaa tgt att ttg ctg att gag gta ttc tgg gcc atc ggg aca gtg ttc	853
Lys Cys Ile Leu Leu Ile Glu Val Phe Trp Ala Ile Gly Thr Val Phe	
210 215 220	
gag gtc gtc ctg gct gtg ttc gtg atg ccc agc ctg ggc tgg cgt tgg	901
Glu Val Val Leu Ala Val Phe Val Met Pro Ser Leu Gly Trp Arg Trp	
225 230 235	
ctg ctc atc ctc tca gct gtc ccg ctc ctc ctc ttt gcc gtg ctg tgt	949
Leu Leu Ile Leu Ser Ala Val Pro Leu Leu Leu Phe Ala Val Leu Cys	
240 245 250 255	
ttc tgg ctg cct gaa agt gca agg tat gat gtg ctg tca ggg aac cag	997
Phe Trp Leu Pro Glu Ser Ala Arg Tyr Asp Val Leu Ser Gly Asn Gln	
260 265 270	
gaa aag gca atc gcc acc tta aag agg ata gca act gaa aac gga gct	1045
Glu Lys Ala Ile Ala Thr Leu Lys Arg Ile Ala Thr Glu Asn Gly Ala	
275 280 285	
ccc atg ccg ctg ggg aaa ctc atc atc tcc aga cag gaa gac cga ggc	1093
Pro Met Pro Leu Gly Lys Leu Ile Ile Ser Arg Gln Glu Asp Arg Gly	
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Lys Met Arg Asp Leu Phe Thr Pro His Phe Arg Trp Thr Thr Leu Leu	
305 310 315	
ctg tgg ttt ata tgg ttt tcc aat gca ttc tct tac tac ggg tta gtt	1189
Leu Trp Phe Ile Trp Phe Ser Asn Ala Phe Ser Tyr Tyr Gly Leu Val	
320 325 330 335	

The following sequence is derived from the

[illegible]

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ctggagccac	atgccccac	ccagcccctn	ttggagtgc	ccgttggtgg	caccaagaga	2468
tccagatgtg	tcctggggac	agctgggtct	tgcaccaggt	gacaacctca	aaacgccgtt	2528
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<400> 2

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Glu	His	Glu	Val	Gln	Ile	Glu	Gly	Val	His	Val	Gly	Leu	Glu	Ala	Val
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Glu	Leu	Asp	Asp	Gly	Ala	Ala	Val	Pro	Lys	Glu	Phe	Ala	Asn	Pro	Thr
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Asp	Asp	Thr	Phe	Met	Val	Glu	Asp	Ala	Val	Glu	Ala	Ile	Gly	Phe	Gly
	65				70					75				80	
Lys	Phe	Gln	Trp	Lys	Leu	Ser	Val	Leu	Thr	Gly	Leu	Ala	Trp	Met	Ala
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Asp	Ala	Met	Glu	Met	Met	Ile	Leu	Ser	Ile	Leu	Ala	Pro	Gln	Leu	His
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Cys	Glu	Trp	Arg	Leu	Pro	Ser	Trp	Gln	Val	Ala	Leu	Leu	Thr	Ser	Val
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Val	Phe	Val	Gly	Met	Met	Ser	Ser	Ser	Thr	Leu	Trp	Gly	Asn	Ile	Ser
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Asp	Gln	Tyr	Gly	Arg	Lys	Thr	Gly	Leu	Lys	Ile	Ser	Val	Leu	Trp	Thr
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Leu	Tyr	Tyr	Gly	Ile	Leu	Ser	Ala	Phe	Ala	Pro	Val	Tyr	Ser	Trp	Ile
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Leu	Val	Leu	Arg	Gly	Leu	Val	Gly	Phe	Gly	Ile	Gly	Gly	Val	Pro	Gln
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Ser	Val	Thr	Leu	Tyr	Ala	Glu	Phe	Leu	Pro	Met	Lys	Ala	Arg	Ala	Lys
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Cys	Ile	Leu	Leu	Ile	Glu	Val	Phe	Trp	Ala	Ile	Gly	Thr	Val	Phe	Glu
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Val	Val	Leu	Ala	Val	Phe	Val	Met	Pro	Ser	Leu	Gly	Trp	Arg	Trp	Leu
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Leu	Ile	Leu	Ser	Ala	Val	Pro	Leu	Leu	Leu	Phe	Ala	Val	Leu	Cys	Phe
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Trp	Leu	Pro	Glu	Ser	Ala	Arg	Tyr	Asp	Val	Leu	Ser	Gly	Asn	Gln	Glu
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Lys	Ala	Ile	Ala	Thr	Leu	Lys	Arg	Ile	Ala	Thr	Glu	Asn	Gly	Ala	Pro
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Met	Pro	Leu	Gly	Lys	Leu	Ile	Ser	Arg	Gln	Glu	Asp	Arg	Gly	Lys	
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Trp	Phe	Ile	Trp	Phe	Ser	Asn	Ala	Phe	Ser	Tyr	Tyr	Gly	Leu	Val	Leu
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Leu	Thr	Thr	Glu	Leu	Phe	Gln	Ala	Gly	Asp	Val	Cys	Gly	Ile	Ser	Ser
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Arg	Lys	Lys	Ala	Val	Glu	Ala	Lys	Cys	Ser	Leu	Ala	Cys	Glu	Tyr	Leu
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Ser	Glu	Glu	Asp	Tyr	Met	Asp	Leu	Leu	Trp	Thr	Thr	Leu	Ser	Glu	Phe
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 35 40 45
 Ser Trp Gln Val Ala Leu Leu Thr Ser Val Val Phe Val Gly Met Met
 50 55 60
 Ser Ser Ser Thr Leu Trp Gly Asn Ile Ser Asp Gln Tyr Gly Arg Lys
 65 70 75 80
 Thr Gly Leu Lys Ile Ser Val Leu Trp Thr Leu Tyr Tyr Gly Ile Leu
 85 90 95
 Ser Ala Phe Ala Pro Val Tyr Ser Trp Ile Leu Val Leu Arg Gly Leu
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 Val Gly Phe Gly Ile Gly Gly Val Pro Gln Ser Val Thr Leu Tyr Ala
 115 120 125
 Glu Phe Leu Pro Met Lys Ala Arg Ala Lys Cys Ile Leu Leu Ile Glu
 130 135 140
 Val Phe Trp Ala Ile Gly Thr Val Phe Glu Val Val Leu Ala Val Phe
 145 150 155 160
 Val Met Pro Ser Leu Gly Trp Arg Trp Leu Leu Ile Leu Ser Ala Val
 165 170 175
 Pro Leu Leu Leu Phe Ala Val Leu Cys Phe Trp Leu Pro Glu Ser Ala
 180 185 190
 Arg Tyr Asp Val Leu Ser Gly Asn Gln Glu Lys Ala Ile Ala Thr Leu
 195 200 205
 Lys Arg Ile Ala Thr Glu Asn Gly Ala Pro Met Pro Leu Gly Lys Leu
 210 215 220
 Ile Ile Ser Arg Gln Glu Asp Arg Gly Lys Met Arg Asp Leu Phe Thr
 225 230 235 240
 Pro His Phe Arg Trp Thr Thr Leu Leu Leu Trp Phe Ile Trp Phe Ser
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 65 70 75 80
 Met Met Val Asn Val Ile Phe Ile Ile Gly Ile Ile Ile Met Ile Phe
 85 90 95
 Ser Ile Asn Tyr Ser Trp Trp Met Tyr Ile Ile Gly Arg Ile Ile Met
 100 105 110
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 115 120 125
 Glu Ile Ala Pro Lys His Leu Arg Gly Thr Met Val Ser Trp Tyr Gln
 130 135 140

Topol 293-000

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 180 185 190
 Pro Glu Ser Pro Arg Trp Leu Val Ile Lys Gly Arg Ile Glu Glu Ala
 195 200 205
 Arg Arg Ser Leu Gln Arg Leu Arg Gly Trp Asp Asp Val Asp Pro Glu
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 Ile Gln Glu Met Met Asp Glu Ile Glu Ala Met Ile Glu Glu Glu Leu
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 Met Arg Trp Arg Ile Ile Met Gly Met Ile Gln Ile Phe Gln Gln
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